Amendments to the Claims

1. (Currently Amended) A hybridization assay probe comprising ~~an oligonucleotide~~ a target binding region from 18 to 35 bases in length that ~~which~~ hybridizes to a target sequence present in target nucleic acid derived from a *Cryptosporidium* ~~organism~~ organisms in a test sample under stringent conditions to form a probe:target hybrid stable for detection, ~~said oligonucleotide having an at least 10 contiguous base region which is at least 80% complementary to an at least 10 contiguous base region present in the target sequence, wherein the~~ said target sequence ~~is~~ being selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3 and SEQ ID NO:4, wherein said probe does not comprise a base region in addition to said target binding region that is capable of stably binding to said target nucleic acid under said conditions, and wherein said probe does not hybridize to nucleic acid derived from a non-*Cryptosporidium* organism in ~~the~~ said test sample to form a probe:non-target hybrid stable for detection under ~~the stringent~~ said conditions.

Claims 2-6 (Canceled)

7. (Currently Amended) The probe of claim 1, wherein said probe contains at least two base ~~sequences which~~ regions that hybridize to each other when said probe is not hybridized to ~~the~~ said target sequence under ~~the stringent~~ said conditions.

8. (Currently Amended) The probe of claim 1, wherein said probe comprises ~~one or more~~ at least one base ~~sequences which~~ region that ~~do~~ does not stably hybridize to nucleic acid derived from *Cryptosporidium* organisms~~, or to nucleic acid derived from a non-target organism present in the test sample,~~ under ~~the stringent~~ said conditions.

9. Canceled

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10. (Original) The probe of claim 1 further comprising a detectable label.

11. (Original) The probe of claim ~~1~~ 7 further comprising a group of interacting labels.

12. (Original) The probe of claim 11, wherein said interacting labels include a luminescent label and a quencher label.

13. (Currently Amended) The probe of claim 1, wherein said ~~oligonucleotide~~ target binding region includes at least one ribonucleotide modified to include a 2'-O-methyl substitution to the ribofuranosyl moiety.

14. (Currently Amended) The probe of claim 1, wherein a pseudo peptide backbone joins at least a portion of the bases of said ~~oligonucleotide~~ target binding region.

15. (Currently Amended) The probe of claim 1, wherein ~~the stringent~~ said conditions comprise 50 mM succinic acid, 1% (w/v) LLS, 7.5 mM aldrithiol-2, 0.6 M LiCl, 115 mM LiOH, 10 mM EDTA, 10 mM EGTA, 1.5% (v/v) ethyl alcohol (absolute), pH to 4.7, and a test sample temperature of about 60°C.

16. (Currently Amended) ~~A hybridization assay~~ The probe of claim 1, ~~comprising an oligonucleotide which hybridizes to a target sequence present in nucleic acid derived from a *Cryptosporidium* organism in a test sample under stringent conditions to form a probe:target hybrid stable for detection,~~ wherein ~~said oligonucleotide has a~~ the base sequence ~~which~~ of said target binding region is at least 80% complementary to the base sequence of ~~the~~ said target sequence~~, wherein the target sequence is selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3 and SEQ ID NO:4, and wherein said probe does not hybridize to nucleic acid derived~~

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~~from a non-*Cryptosporidium* organism in the test sample to form a probe:non-target hybrid stable for detection under the stringent conditions.~~

17. (Currently Amended) ~~An oligonucleotide~~ The probe of claim 1, ~~which hybridizes to a target sequence present in nucleic acid derived from a *Cryptosporidium* organism in a test sample under stringent conditions to form a probe:target hybrid stable for detection,~~ wherein the base sequence of said probe is at least 80% complementary to the base sequence of the said target sequence, ~~wherein the target sequence is selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3 and SEQ ID NO:4, and wherein said probe does not hybridize to nucleic acid derived from a non-*Cryptosporidium* organism in the test sample to form a probe:non-target hybrid stable for detection under the stringent conditions.~~

18. (Currently Amended) ~~An oligonucleotide~~ The probe of claim 1, ~~which hybridizes to a target sequence present in nucleic acid derived from a *Cryptosporidium* organism in a test sample under stringent conditions to form a probe:target hybrid stable for detection,~~ wherein the base sequence of said probe is fully complementary to the base sequence of the said target sequence, ~~wherein the target sequence is selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3 and SEQ ID NO:4, and wherein said probe does not hybridize to nucleic acid derived from a non-*Cryptosporidium* organism in the test sample to form a probe:non-target hybrid stable for detection under the stringent conditions.~~

19. (Currently Amended) A probe mix comprising the said probe of claim 1 and a first helper oligonucleotide from 18 to 35 bases in length which hybridizes to ~~having an at least 10 contiguous base region which is at least 80% complementary to an at least 10 contiguous base region present in~~ a target sequence, ~~wherein the target sequence of said first helper oligonucleotide is~~ selected from the group consisting of SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25 and SEQ ID NO:27 under said conditions.

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20. Canceled

21. (Withdrawn) The probe mix of claim 19 further comprising a second helper oligonucleotide having an at least 10 contiguous base region which is at least 80% complementary to an at least 10 contiguous base region present in a target sequence, wherein the target sequence of said second helper oligonucleotide is selected from the group consisting of SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26 and SEQ ID NO:28.

22. Canceled

23. (Currently Amended) An amplification ~~primer~~ oligonucleotide for use in amplifying a nucleic acid sequence present in target nucleic acid derived from a *Cryptosporidium* ~~organism~~ organisms ~~under amplification conditions~~, said ~~primer~~ amplification oligonucleotide comprising a target binding region from 18 to 40 bases in length which hybridizes to ~~an oligonucleotide having an at least 10 contiguous base region which is at least 80% complementary to an at least 10 contiguous base region present in~~ a target sequence selected from the group consisting of SEQ ID NO:48, SEQ ID NO:54, SEQ ID NO:60 and SEQ ID NO:66 under amplification conditions, wherein said amplification oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to said target nucleic acid under said conditions, and wherein said ~~primer~~ amplification oligonucleotide optionally includes a 5' sequence ~~which~~ that is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

Claims 24-32 (Canceled)

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33. (Currently Amended) The ~~primer~~ amplification oligonucleotide of claim 23, wherein said ~~primer~~ amplification oligonucleotide includes ~~the~~ said 5' sequence ~~which is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.~~

34. (Currently Amended) The ~~primer~~ amplification oligonucleotide of claim 33, wherein ~~the~~ said 5' sequence ~~which is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase~~ is a T7 promoter having the base sequence of SEQ ID NO:69.

35. (Currently Amended) The primer amplification oligonucleotide of claim 23, wherein said primer amplification oligonucleotide contains at least two base ~~sequences which~~ regions that hybridize to each other when said amplification oligonucleotide is not hybridized to ~~the~~ said target sequence under ~~the amplification~~ said conditions.

36. (Currently Amended) The ~~primer~~ amplification oligonucleotide of claim 35 further comprising a group of interacting labels.

37. (Currently Amended) The ~~primer~~ amplification oligonucleotide of claim 36, wherein said interacting labels include a luminescent label and a quencher label.

38. (Currently Amended) ~~An~~ The amplification oligonucleotide of claim 23, wherein the base sequence of said target binding region ~~primer for use in amplifying a nucleic acid sequence present in nucleic acid derived from a *Cryptosporidium* organism under amplification conditions, said primer comprising an oligonucleotide having a base sequence which~~ is at least 80% complementary to the base sequence of a said target sequence~~, selected from the group consisting of SEQ ID NO:48, SEQ ID NO:54, SEQ ID NO:60 and SEQ ID NO:66, and wherein said primer~~

~~optionally includes a 5' sequence which is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.~~

39. Canceled

40. (Currently Amended) ~~An~~ The amplification oligonucleotide of claim 23, wherein the base sequence of said target binding region ~~primer for use in amplifying a nucleic acid sequence present in nucleic acid derived from a *Cryptosporidium* organism under amplification conditions, wherein the base sequence of said primer~~ is fully complementary to the base sequence of a said target sequence ~~selected from the group consisting of SEQ ID NO:48, SEQ ID NO:54, SEQ ID NO:60 and SEQ ID NO:66, and wherein said oligonucleotide optionally includes a 5' sequence which is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.~~

41. (Currently Amended) A set of amplification ~~primers~~ oligonucleotides for use in amplifying a nucleic acid sequence present in target nucleic acid derived from a *Cryptosporidium* ~~organism~~ organisms ~~under amplification conditions~~, said set of primers amplification oligonucleotides including first and second primers amplification oligonucleotides, wherein:

said first ~~primer~~ amplification oligonucleotide is said ~~primer~~ amplification oligonucleotide of claim 23; and

said second ~~primer~~ amplification oligonucleotide comprises a target binding region from 18 to 40 bases in length which hybridizes to ~~an oligonucleotide having an at least 10 contiguous base region which is at least 80% complementary to an at least 10 contiguous base region present in~~ a target sequence selected from the group consisting of SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:63 and SEQ ID NO:64 under amplification conditions, wherein said second amplification oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to said target

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nucleic acid under said conditions, and wherein ~~one or more primers~~ said second amplification oligonucleotide ~~of said set of primers~~ optionally ~~include~~ includes a 5' sequence ~~which~~ that is recognized by an RNA polymerase or ~~which~~ that enhances initiation or elongation by an RNA polymerase.

42. Canceled

43. (Currently Amended) The ~~primer~~ set of amplification oligonucleotides of claim 41, wherein ~~the~~ said target sequence of said second ~~primer~~ amplification oligonucleotide is selected from the group consisting of SEQ ID NO:45, SEQ ID NO:51, SEQ ID NO:57 and SEQ ID NO:63.

44. Canceled

45. (Currently Amended) The ~~primer~~ set of amplification oligonucleotides of claim 41, wherein ~~the~~ said target sequence of said second ~~primer~~ amplification oligonucleotide is selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64.

Claims 46-49 (Canceled)

50. (Currently Amended) A method for determining the presence of a *Cryptosporidium* ~~organism~~ organisms in a test sample, said method comprising the steps of:

contacting ~~the~~ said test sample with said probe of claim 1 under stringent conditions; and

determining whether a probe:target hybrid has formed as an indication of the presence of a *Cryptosporidium* ~~organism~~ organisms in ~~the~~ said test sample.

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51. (Currently Amended) A method for determining the presence of ~~a~~ *Cryptosporidium* ~~organism~~ organisms in a test sample, said method comprising the steps of:

contacting ~~the~~ said test sample with said probe of claim 16 under stringent conditions; and

determining whether a probe:target hybrid has formed as an indication of the presence of ~~a~~ *Cryptosporidium* ~~organism~~ organisms in ~~the~~ said test sample.

52. (Currently Amended) A method for determining the presence of ~~a~~ *Cryptosporidium* ~~organism~~ organisms in a test sample, said method comprising the steps of:

contacting ~~the~~ said test sample with said probe of claim 17 under stringent conditions; and

determining whether a probe:target hybrid has formed as an indication of the presence of ~~a~~ *Cryptosporidium* ~~organism~~ organisms in ~~the~~ said test sample.

53. (Currently Amended) A method for determining the presence of ~~a~~ *Cryptosporidium* ~~organism~~ organisms in a test sample, said method comprising the steps of:

contacting ~~the~~ said test sample with said probe of claim 18 under stringent conditions; and

determining whether a probe:target hybrid has formed as an indication of the presence of ~~a~~ *Cryptosporidium* ~~organism~~ organisms in ~~the~~ said test sample.

54. (Currently Amended) A method for amplifying *Cryptosporidium* nucleic acid ~~which~~ that may be present in a test sample, said method comprising the steps of:

contacting ~~the~~ said test sample with said ~~primer~~ amplification oligonucleotide of claim 23 under amplification conditions; and

amplifying a target sequence present in target nucleic acid derived from ~~a~~ *Cryptosporidium* ~~organism which~~ organisms that may be present in ~~the~~ said test sample.

Claims 55-60 (Canceled)

61. (Currently Amended) The method of claim 54 further comprising the step of providing to said test sample a hybridization assay probe for use in determining ~~the presence of the~~ whether said target sequence was amplified in said amplifying step ~~target sequence in the test sample with a hybridization assay probe~~.

62. (Currently Amended) The method of claim 61, wherein said probe comprises ~~an oligonucleotide which~~ a target binding region from 18 to 35 bases in length that hybridizes to ~~the amplified~~ said target sequence or the complement thereof under stringent conditions to form a probe:target hybrid stable for detection, ~~said oligonucleotide having an at least 10 contiguous base region which is at least 80% complementary to an at least 10 contiguous base region present in the amplified target sequence, wherein the amplified~~ said target sequence or the complement thereof ~~is~~ being selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3 and SEQ ID NO:4, wherein said probe does not comprise a base region in addition to said target binding region that is capable of stably binding to nucleic acid derived from *Cryptosporidium* organisms under said conditions, and wherein said probe does not hybridize to nucleic acid derived from a non-*Cryptosporidium* organism in ~~the~~ said test sample to form a probe:non-target hybrid stable for detection under ~~the stringent~~ said conditions.

Claims 63-70 (Canceled)

71. (Currently Amended) A method for amplifying *Cryptosporidium* nucleic acid ~~which~~ that may be present in a test sample, said method comprising the steps of:

contacting ~~the~~ said test sample with said primer amplification oligonucleotide of claim 38 under amplification conditions; and

amplifying a target sequence present in target nucleic acid derived from a *Cryptosporidium* ~~organism which~~ organisms that may be present in ~~the~~ said test sample.

72. Canceled

73. (Currently Amended) A method for amplifying *Cryptosporidium* nucleic acid ~~which~~ that may be present in a test sample, said method comprising the steps of:

contacting ~~the~~ said test sample with said ~~primer~~ amplification oligonucleotide of claim 40 under amplification conditions; and

amplifying a target sequence present in target nucleic acid derived from ~~a~~ *Cryptosporidium* ~~organism which~~ organisms that may be present in ~~the~~ said test sample.

74. (Currently Amended) A kit comprising, in packaged combination, first and second oligonucleotides for use in determining the presence of ~~a~~ *Cryptosporidium* ~~organism~~ organisms in a test sample, each of said oligonucleotides comprising a target binding region ~~having an at least 10 contiguous base region which is at least 80% complementary to an at least 10 contiguous base region present in~~ which hybridizes to a target sequence ~~contained~~ present in target nucleic acid derived from ~~a~~ *Cryptosporidium* ~~organism~~ organisms under hybridization conditions, said target binding region of said first oligonucleotide being from 18 to 35 bases in length and said target binding region of said second oligonucleotide being from 18 to 40 bases in length,

wherein: ~~the~~ said target sequence of said first oligonucleotide is selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3 and SEQ ID NO:4,;

~~the~~ wherein said target sequence of said second oligonucleotide is selected from the group consisting of SEQ ID NO:48, SEQ ID NO:54, SEQ ID NO:60 and SEQ ID NO:66,; ~~and~~

wherein neither of said first and second oligonucleotides comprises a base region in addition to said target binding region that is capable of stably binding to said target nucleic acid under said conditions, and

wherein said second oligonucleotide optionally includes a 5' sequence ~~which~~ that is recognized by an RNA polymerase or ~~which~~ that enhances initiation or elongation by an RNA polymerase.

Claims 75-82 (Canceled)

83. (Currently Amended) The kit of claim 74 further comprising a third oligonucleotide, ~~wherein said third oligonucleotide has an at least 10 contiguous base region which is at least 80% complementary to an at least 10 contiguous base region present in~~ said third oligonucleotide comprising a target binding region from 18 to 40 bases in length which hybridizes to a target sequence ~~contained~~ present in target nucleic acid derived from ~~a~~ *Cryptosporidium* ~~organism~~ organisms under hybridization conditions, ~~and wherein the~~ said target sequence ~~of said third oligonucleotide is~~ being selected from the group consisting of SEQ ID NO:45, SEQ ID NO:51, SEQ ID NO:57 and SEQ ID NO:63, wherein said third oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to said target nucleic acid under said conditions, and wherein said third oligonucleotide optionally includes a 5' sequence that is recognized by an RNA polymerase or that enhances initiation or elongation by an RNA polymerase.

84. Canceled

85. (Currently Amended) The kit of claim 74 further comprising a third oligonucleotide, ~~wherein said third oligonucleotide has an at least 10 contiguous base region which is at least 80% complementary to an at least 10 contiguous base region present in~~ said third oligonucleotide comprising a target binding region from 18 to 40 bases in length which hybridizes to a target sequence ~~contained~~ present in target nucleic acid derived from ~~a~~ *Cryptosporidium* ~~organism~~ organisms under hybridization conditions, ~~and wherein the~~ said target sequence ~~of said~~

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~~third oligonucleotide is~~ being selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64, wherein said third oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to said target nucleic acid under said conditions, and wherein said third oligonucleotide optionally includes a 5' sequence that is recognized by an RNA polymerase or that enhances initiation or elongation by an RNA polymerase.

Claims 86 and 87 (Canceled)

88. (Currently Amended) A kit comprising, in packaged combination, first and second oligonucleotides for use in determining the presence of a *Cryptosporidium* ~~organism~~ organisms in a test sample, each of said oligonucleotides comprising a target binding region from 18 to 35 bases in length ~~having an at least 10 contiguous base region which is at least 80% complementary to an at least 10 contiguous base region present in~~ that hybridizes to a target sequence ~~contained~~ present in target nucleic acid derived from a *Cryptosporidium* ~~organism~~ organisms under stringent conditions,

wherein: ~~the~~ said target sequence of said first oligonucleotide is selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3 and SEQ ID NO:4, ~~; and~~

~~the~~ wherein said target sequence of said second oligonucleotide is selected from the group consisting of SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25 and SEQ ID NO:27,

wherein neither of said first and second oligonucleotides comprises a base region in addition to said target binding region that is capable of stably binding to said target nucleic acid under said conditions, and

wherein said first oligonucleotide does not hybridize to nucleic acid derived from a non-*Cryptosporidium* organism in said test sample to form a probe:non-target hybrid stable for detection under said conditions.

Claims 89-91 (Canceled)

92. (Currently Amended) The probe of claim ~~16~~ 1, wherein ~~said oligonucleotide has a~~ the base sequence of said target binding region is fully ~~which is 100%~~ complementary to the base sequence of ~~the~~ said target sequence.

93. (Currently Amended) A probe mix comprising ~~the~~ said probe of claim 16 and a first helper oligonucleotide, wherein the base sequence of said first helper oligonucleotide is at least 80% complementary to the base sequence of a target sequence selected from the group consisting of SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25 and SEQ ID NO:27.

94. (Previously Added) The probe mix of claim 93 further comprising a second helper oligonucleotide, wherein the base sequence of said second helper oligonucleotide is at least 80% complementary to the base sequence of a target sequence selected from the group consisting of SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26 and SEQ ID NO:28.

95. (Currently Amended) A probe mix comprising ~~the~~ said probe of claim 17 and a first helper oligonucleotide, wherein the base sequence of said first helper oligonucleotide is at least 80% complementary to the base sequence of a target sequence selected from the group consisting of SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25 and SEQ ID NO:27.

96. (Previously Added) The probe mix of claim 95 further comprising a second helper oligonucleotide, wherein the base sequence of said second helper oligonucleotide is at least 80% complementary to the base sequence of a target sequence selected from the group consisting of SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26 and SEQ ID NO:28.

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97. (Currently Amended) A probe mix comprising ~~the~~ said probe of claim 18 and a first helper oligonucleotide, wherein the base sequence of said first helper oligonucleotide is fully complementary to the base sequence of a target sequence selected from the group consisting of SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25 and SEQ ID NO:27.

98. (Previously Added) The probe mix of claim 97 further comprising a second helper oligonucleotide, wherein the base sequence of said second helper oligonucleotide is fully complementary to the base sequence of a target sequence selected from the group consisting of SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26 and SEQ ID NO:28.

99. (Currently Amended) The ~~primer~~ amplification oligonucleotide of claim 38, wherein ~~said oligonucleotide has a~~ the base sequence of said target binding region ~~which is 100%~~ is fully complementary to the base sequence of ~~the~~ said target sequence.

100. (Currently Amended) A set of amplification ~~primers~~ oligonucleotides for use in amplifying a nucleic acid sequence present in target nucleic acid derived from a *Cryptosporidium* ~~organism~~ organisms under ~~amplification conditions~~, said set of ~~primers~~ amplification oligonucleotides including first and second ~~primers~~ amplification oligonucleotides, wherein:

said first ~~primer~~ amplification oligonucleotide is said ~~primer~~ amplification oligonucleotide of claim 38; and

said second ~~primer~~ amplification oligonucleotide comprises ~~an oligonucleotide having~~ a target binding region, wherein the base sequence ~~which~~ of said target binding region is at least 80% complementary to the base sequence of a target sequence selected from the group consisting of SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:63 and SEQ ID NO:64,

wherein said target binding region of said second amplification oligonucleotide hybridizes to said target sequence under amplification conditions.

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wherein said second amplification oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to said target nucleic acid under said conditions, and

wherein said second amplification oligonucleotide optionally includes a 5' sequence that is recognized by an RNA polymerase or that enhances initiation or elongation by an RNA polymerase.

101. (Currently Amended) The ~~primer~~ set of amplification oligonucleotides of claim 100, wherein the said target sequence of said second ~~primer~~ amplification oligonucleotide is selected from the group consisting of SEQ ID NO:45, SEQ ID NO:51, SEQ ID NO:57 and SEQ ID NO:63.

102. (Currently Amended) The ~~primer~~ set of amplification oligonucleotides of claim 100, wherein the said target sequence of said second primer amplification oligonucleotide is selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64.

Claims 103-105 (Canceled)

106. (Currently Amended) A set of amplification ~~primers~~ oligonucleotides for use in amplifying a nucleic acid sequence present in target nucleic acid derived from a *Cryptosporidium* ~~organism~~ organisms ~~under amplification conditions~~, said set of ~~primers~~ amplification oligonucleotides including first and second primers amplification oligonucleotides, wherein:

said first primer amplification oligonucleotide is said primer amplification oligonucleotide of claim 40; and

said second primer amplification oligonucleotide comprises ~~an oligonucleotide~~ a target binding region, wherein the base sequence of said primer target binding region is fully

complementary to the base sequence of a target sequence selected from the group consisting of SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:63 and SEQ ID NO:64,

wherein said target binding region of said second amplification oligonucleotide hybridizes to said target sequence under amplification conditions,

wherein said second amplification oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to said target nucleic acid under said conditions, and

wherein said second amplification oligonucleotide optionally includes a 5' sequence that is recognized by an RNA polymerase or that enhances initiation or elongation by an RNA polymerase.

107. (Currently Amended) The ~~primer~~ set of amplification oligonucleotides of claim 106, wherein ~~the~~ said target sequence of said second ~~primer~~ amplification oligonucleotide is selected from the group consisting of SEQ ID NO:45, SEQ ID NO:51, SEQ ID NO:57 and SEQ ID NO:63.

108. (Currently Amended) The ~~primer~~ set of amplification oligonucleotides of claim 106, wherein ~~the~~ said target sequence of said second ~~primer~~ amplification oligonucleotide is selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64.

109. (Currently Amended) The method of claim 51, wherein ~~said oligonucleotide has a~~ the base sequence ~~which is 100%~~ of said target binding region is fully complementary to the base sequence of ~~the~~ said target sequence.

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110. (Currently Amended) The method of claim 54 further comprising a second amplification ~~primer~~ oligonucleotide, said second ~~primer~~ amplification oligonucleotide comprising a target binding region from 18 to 40 bases in length that hybridizes to ~~an oligonucleotide having an at least 10 contiguous base region which is at least 80% complementary to an at least 10 contiguous base region present in~~ a target sequence selected from the group consisting of SEQ ID NO:45, SEQ ID NO:51, SEQ ID NO:57 and SEQ ID NO:63 under said conditions, wherein said second amplification oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to said target nucleic acid under said conditions, and wherein said second amplification oligonucleotide optionally includes a 5' sequence that is recognized by an RNA polymerase or that enhances initiation or elongation by an RNA polymerase.

111. (Currently Amended) The method of claim 110 further comprising the step of determining the presence of ~~the~~ amplicon ~~amplified target sequence~~ in ~~a~~ said test sample with a hybridization assay probe, wherein said probe comprises ~~an oligonucleotide which~~ a target binding region from 18 to 35 bases in length that hybridizes to ~~the~~ a target sequence present in said amplicon ~~amplified target sequence~~ under stringent conditions to form a probe:target hybrid stable for detection, ~~said oligonucleotide having an at least 10 contiguous base region which is at least 80% complementary to an at least 10 contiguous base region present in the amplified target sequence, wherein the~~ said ~~amplified~~ target sequence ~~is~~ being selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3 and SEQ ID NO:4, wherein said probe does not comprise a base region in addition to said target binding region that is capable of stably binding to said amplicon under said conditions, and wherein said probe does not hybridize to nucleic acid derived from a non-*Cryptosporidium* organism in the said test sample to form a probe:non-target hybrid stable for detection under ~~the stringent~~ said conditions.

112. (Currently Amended) The method of claim 54 further comprising a second amplification ~~primer~~ oligonucleotide, said second ~~primer~~ amplification oligonucleotide comprising

a target binding region from 18 to 40 bases in length that hybridizes to ~~an oligonucleotide having an at least 10 contiguous base region which is at least 80% complementary to an at least 10 contiguous base region present in~~ a target sequence selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64 under said conditions, wherein said second amplification oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to said target nucleic acid under said conditions, and wherein said second amplification oligonucleotide optionally includes a 5' sequence that is recognized by an RNA polymerase or that enhances initiation or elongation by an RNA polymerase.

113. (Currently Amended) The method of claim 112 further comprising the step of determining the presence of ~~the~~ amplicon ~~amplified target sequence~~ in a said test sample with a hybridization assay probe, wherein said probe comprises ~~an oligonucleotide which~~ a target binding region from 18 to 35 bases in length that hybridizes to ~~the~~ a target sequence present in said amplicon ~~amplified target sequence~~ under stringent conditions to form a probe:target hybrid stable for detection, ~~said oligonucleotide having an at least 10 contiguous base region which is at least 80% complementary to an at least 10 contiguous base region present in the amplified target sequence, wherein the~~ said ~~amplified~~ target sequence ~~is~~ being selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3 and SEQ ID NO:4, wherein said probe does not comprise a base region in addition to said target binding region that is capable of stably binding to said amplicon under said conditions, and wherein said probe does not hybridize to nucleic acid derived from a non-*Cryptosporidium* organism in ~~the~~ said test sample to form a probe:non-target hybrid stable for detection under ~~the stringent~~ said conditions.

114. (Currently Amended) The method of claim 71 further comprising the step of determining the presence of ~~the~~ amplicon ~~amplified target sequence~~ in a said test sample with a hybridization assay probe, wherein said probe comprises ~~an oligonucleotide which~~ a target binding region that hybridizes to ~~the~~ a target sequence present in said amplicon ~~amplified target sequence~~

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under stringent conditions to form a probe:target hybrid stable for detection, wherein ~~said oligonucleotide has a~~ the base sequence of said target binding region ~~which~~ is at least 80% complementary to the base sequence of said target sequence ~~amplified target sequence, wherein the~~ said target ~~amplified target sequence is~~ being selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3 and SEQ ID NO:4, wherein said probe does not comprise a base region in addition to said target binding region that is capable of stably binding to said amplicon under said conditions, and wherein said probe does not hybridize to nucleic acid derived from a non-*Cryptosporidium* organism in ~~the~~ said test sample to form a probe:non-target hybrid stable for detection under ~~the stringent~~ said conditions.

115. (Currently Amended) The method of claim 71 further comprising a second amplification ~~primer~~ oligonucleotide, ~~said second primer~~ comprising ~~an oligonucleotide having~~ a target binding region, wherein the ~~a~~ base sequence of said target binding region ~~which~~ is at least 80% complementary to a the base sequence of a target sequence present in target nucleic acid derived from *Cryptosporidium* organisms, said target sequence being selected from the group consisting of SEQ ID NO:45, SEQ ID NO:51, SEQ ID NO:57 and SEQ ID NO:63,

wherein said target binding region hybridizes to said target sequence under said conditions,

wherein said second amplification oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to said target nucleic acid under said conditions, and

wherein said second amplification oligonucleotide optionally includes a 5' sequence that is recognized by an RNA polymerase or that enhances initiation or elongation by an RNA polymerase.

116. (Currently Amended) The method of claim 115 further comprising the step of determining the presence of ~~the~~ amplicon ~~amplified target sequence~~ in ~~a~~ said test sample with a

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hybridization assay probe, wherein said probe comprises ~~an oligonucleotide which~~ a target binding region that hybridizes to ~~the~~ a target sequence present in said amplicon ~~amplified target sequence~~ under stringent conditions to form a probe:target hybrid stable for detection, wherein ~~said oligonucleotide has a~~ the base sequence of said target binding region ~~which~~ is at least 80% complementary to the base sequence of said target sequence ~~amplified target sequence, wherein the~~ said ~~amplified~~ target sequence ~~is~~ being selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3 and SEQ ID NO:4, wherein said probe does not comprise a base region in addition to said target binding region that is capable of stably binding to said amplicon under said conditions, and wherein said probe does not hybridize to nucleic acid derived from a non-*Cryptosporidium* organism in the said test sample to form a probe:non-target hybrid stable for detection under ~~the stringent~~ said conditions.

117. (Currently Amended) The method of claim 71 further comprising a second amplification ~~primer~~ oligonucleotide, ~~said second primer~~ comprising ~~an oligonucleotide having~~ a target binding region, wherein ~~the~~ a base sequence of said target binding region ~~which~~ is at least 80% complementary to a the base sequence of a target sequence present in target nucleic acid derived from *Cryptosporidium* organisms, said target sequence being selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64,

wherein said target binding region hybridizes to said target sequence under said conditions,

wherein said second amplification oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to said target nucleic acid under said conditions, and

wherein said second amplification oligonucleotide optionally includes a 5' sequence that is recognized by an RNA polymerase or that enhances initiation or elongation by an RNA polymerase.

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118. (Currently Amended) The method of claim 117 further comprising the step of determining the presence of ~~the~~ amplicon ~~amplified target sequence~~ in ~~a~~ said test sample with a hybridization assay probe, wherein said probe comprises ~~an oligonucleotide which~~ a target binding region that hybridizes to ~~the~~ a target sequence present in said amplicon ~~amplified target sequence~~ under stringent conditions to form a probe:target hybrid stable for detection, wherein ~~said oligonucleotide has a~~ the base sequence of said target binding region ~~which~~ is at least 80% complementary to the base sequence of said ~~amplified~~ target sequence, ~~wherein the~~ said ~~amplified~~ target sequence ~~is~~ being selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3 and SEQ ID NO:4, wherein said probe does not comprise a base region in addition to said target binding region that is capable of stably binding to said amplicon under said conditions, and wherein said probe does not hybridize to nucleic acid derived from a non-*Cryptosporidium* organism in ~~the~~ said test sample to form a probe:non-target hybrid stable for detection under ~~the stringent~~ said conditions.

119. (Currently Amended) The method of claim 71, wherein ~~said oligonucleotide has a~~ the base sequence ~~which~~ of said target binding region is ~~100%~~ fully complementary to the base sequence of ~~the~~ said target sequence.

120. (Currently Amended) The method of claim 119 further comprising the step of determining the presence of ~~the~~ amplicon ~~amplified target sequence~~ in ~~a~~ said test sample with a hybridization assay probe, wherein said probe comprises ~~an oligonucleotide which~~ a target binding region that hybridizes to ~~the~~ a target sequence present in said amplicon ~~amplified target sequence~~ under stringent conditions to form a probe:target hybrid stable for detection, wherein the base sequence of said ~~oligonucleotide~~ target binding region ~~has a base sequence which~~ is ~~100%~~ fully complementary to the base sequence of said ~~amplified~~ target sequence, ~~wherein the~~ said ~~amplified~~ target sequence ~~is~~ being selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3 and SEQ ID NO:4, wherein said probe does not comprise a base region in addition to said

target binding region that is capable of stably binding to said amplicon under said conditions, and wherein said probe does not hybridize to nucleic acid derived from a non-*Cryptosporidium* organism in the said test sample to form a probe:non-target hybrid stable for detection under ~~the stringent~~ said conditions.

121. (Currently Amended) The method of claim 119 further comprising a second amplification ~~primer~~ oligonucleotide, ~~said second primer~~ comprising ~~an oligonucleotide having~~ a target binding region, wherein the a base sequence ~~which~~ of said target binding region is ~~100%~~ fully complementary to a the base sequence of a target sequence present in target nucleic acid derived from *Cryptosporidium* organisms, said target sequence being selected from the group consisting of SEQ ID NO:45, SEQ ID NO:51, SEQ ID NO:57 and SEQ ID NO:63,

wherein said target binding region hybridizes to said target sequence under said conditions,

wherein said second amplification oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to said target nucleic acid under said conditions, and

wherein said second amplification oligonucleotide optionally includes a 5' sequence that is recognized by an RNA polymerase or that enhances initiation or elongation by an RNA polymerase.

122. (Currently Amended) The method of claim 121 further comprising the step of determining the presence of ~~the~~ amplicon ~~amplified target sequence~~ in a test sample with a hybridization assay probe, wherein said probe comprises ~~an oligonucleotide which~~ a target binding region that hybridizes to ~~the~~ a target sequence present in said amplicon ~~amplified target sequence~~ under stringent conditions to form a probe:target hybrid stable for detection, wherein said ~~oligonucleotide~~ the base sequence of said target binding region ~~has a base sequence which~~ is ~~100%~~ fully complementary to the base sequence of said ~~amplified~~ target sequence, ~~wherein the~~ said

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~~amplified~~ target sequence ~~is~~ being selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3 and SEQ ID NO:4, wherein said probe does not comprise a base region in addition to said target binding region that is capable of stably binding to said amplicon under said conditions, and wherein said probe does not hybridize to nucleic acid derived from a non-*Cryptosporidium* organism in ~~the~~ said test sample to form a probe:non-target hybrid stable for detection under ~~the stringent~~ said conditions.

123. (Currently Amended) The method of claim 119 further comprising a second amplification ~~primer~~ oligonucleotide, ~~said second primer~~ comprising ~~an oligonucleotide~~ a target binding region, wherein the base sequence of said target binding region ~~having a base sequence which~~ is ~~100%~~ fully complementary to ~~a~~ the base sequence of a target sequence present in target nucleic acid derived from *Cryptosporidium* organisms, said target sequence being selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64,

wherein said target binding region hybridizes to said target sequence under said conditions,

wherein said second amplification oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to said target nucleic acid under said conditions, and

wherein said second amplification oligonucleotide optionally includes a 5' sequence that is recognized by an RNA polymerase or that enhances initiation or elongation by an RNA polymerase.

124. (Currently Amended) The method of claim 123 further comprising the step of determining the presence of ~~the~~ amplicon ~~amplified target sequence~~ in a said test sample with a hybridization assay probe, wherein said probe comprises ~~an oligonucleotide which~~ a target binding region that hybridizes to ~~the~~ a target sequence present in said amplicon ~~amplified target sequence~~ under stringent conditions to form a probe:target hybrid stable for detection, wherein the base

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sequence of said ~~oligonucleotide~~ target binding region ~~has a base sequence which~~ is ~~100%~~ fully complementary to the base sequence of said ~~amplified~~ target sequence, ~~wherein the~~ said ~~amplified~~ target sequence ~~is~~ being selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3 and SEQ ID NO:4, wherein said probe does not comprise a base region in addition to said target binding region that is capable of stably binding to said amplicon under said conditions, and wherein said probe does not hybridize to nucleic acid derived from a non-*Cryptosporidium* organism in ~~the~~ said test sample to form a probe:non-target hybrid stable for detection under ~~the stringent~~ said conditions.

Claims 125-129 (Canceled)

130. (Currently Amended) The method of claim 73 further comprising the step of determining the presence of ~~the~~ amplicon ~~amplified target sequence~~ in ~~a~~ said test sample with an oligonucleotide probe, wherein the base sequence of said probe is fully complementary to the base sequence of ~~the~~ a ~~amplified~~ target sequence present in said amplicon, ~~and wherein the~~ said ~~amplified~~ target sequence ~~is~~ being selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3 and SEQ ID NO:4.

131. (Currently Amended) The method of claim 73 further comprising a second amplification ~~primer~~ oligonucleotide, comprising a target binding region, wherein the base sequence of said ~~second primer~~ target binding region is fully complementary to a the base sequence of a target sequence present in target nucleic acid derived from *Cryptosporidium* organisms, said target sequence being selected from the group consisting of SEQ ID NO:45, SEQ ID NO:51, SEQ ID NO:57 and SEQ ID NO:63,

wherein said target binding region hybridizes to said target sequence under said conditions.

wherein said second amplification oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to said target nucleic acid under said conditions, and

wherein said second amplification oligonucleotide optionally includes a 5' sequence that is recognized by an RNA polymerase or that enhances initiation or elongation by an RNA polymerase.

132. (Currently Amended) The method of claim 131 further comprising the step of determining the presence of ~~the~~ amplicon ~~amplified target sequence~~ in a said test sample with an oligonucleotide probe, wherein the base sequence of said probe is fully complementary to the base sequence of ~~the~~ a ~~amplified~~ target sequence present in said amplicon, ~~and wherein the~~ said ~~amplified~~ target sequence ~~is~~ being selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3 and SEQ ID NO:4.

133. (Currently Amended) The method of claim 73 further comprising a second amplification ~~primer~~ oligonucleotide, comprising a target binding region, wherein the base sequence of said ~~second primer~~ target binding region is fully complementary to a the base sequence of a target sequence present in target nucleic acid derived from *Cryptosporidium* organisms, said target sequence being selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64,

wherein said target binding region hybridizes to said target sequence under said conditions,

wherein said second amplification oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to said target nucleic acid under said conditions, and

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wherein said second amplification oligonucleotide optionally includes a 5' sequence that is recognized by an RNA polymerase or that enhances initiation or elongation by an RNA polymerase.

134. (Currently Amended) The method of claim 133 further comprising the step of determining the presence of ~~the~~ amplicon ~~amplified target sequence~~ in a said test sample with an oligonucleotide probe, wherein the base sequence of said probe is fully complementary to the base sequence of ~~the~~ a ~~amplified~~ target sequence present in said amplicon, ~~and wherein the~~ said ~~amplified~~ target sequence ~~is~~ being selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3 and SEQ ID NO:4.

135. (Currently Amended) The kit of claim 74, wherein ~~each of said oligonucleotides has a base region which~~ the base sequence of said target binding region of each said oligonucleotide is at least 80% complementary to the base sequence of ~~the~~ said target sequence of said oligonucleotide.

136. (Currently Amended) The kit of claim 74, wherein ~~each of said oligonucleotides has a base region which is 100%~~ the base sequence of said target binding region of each said oligonucleotide is fully complementary to the base sequence of ~~the~~ said target sequence of said oligonucleotide.

137. (Currently Amended) The kit of claim 74, wherein the base sequence of each of said ~~oligonucleotides~~ oligonucleotide is at least 80% complementary to the base sequence of ~~the~~ said target sequence of said oligonucleotide.

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138. (Currently Amended) The kit of claim 74, wherein the base sequence ~~of each~~ of each said ~~oligonucleotides~~ oligonucleotide is fully complementary to the base sequence of ~~the~~ said target sequence of said oligonucleotide.

139. (Currently Amended) The kit of claim 83, wherein ~~each of said oligonucleotides has a base region which~~ the base sequence of said target binding region of each said oligonucleotide is at least 80% complementary to the base sequence of ~~the~~ said target sequence of said oligonucleotide.

140. (Currently Amended) The kit of claim 83, wherein ~~each of said oligonucleotides has a base region which is 100%~~ the base sequence of said target binding region of each said oligonucleotide is fully complementary to the base sequence of ~~the~~ said target sequence of said oligonucleotide.

141. (Currently Amended) The kit of claim 83, wherein the base sequence of each of said ~~oligonucleotides~~ oligonucleotide is at least 80% complementary to the base sequence of ~~the~~ said target sequence of said oligonucleotide.

142. (Currently Amended) The kit of claim 83, wherein the base sequence of each of said ~~oligonucleotides~~ oligonucleotide is fully complementary to the base sequence of ~~the~~ said target sequence of said oligonucleotide.

143. (Currently Amended) The kit of claim 85, wherein ~~each of said oligonucleotides has a base region which~~ the base sequence of said target binding region of each said oligonucleotide is at least 80% complementary to the base sequence of ~~the~~ said target sequence of said oligonucleotide.

144. (Currently Amended) The kit of claim 85, wherein ~~each of said oligonucleotides has a base region which is 100%~~ the base sequence of said target binding region of each said oligonucleotide is fully complementary to the base sequence of ~~the~~ said target sequence of said oligonucleotide.

145. (Currently Amended) The kit of claim 85, wherein the base sequence of each ~~of~~ said ~~oligonucleotides~~ oligonucleotide is at least 80% complementary to the base sequence of ~~the~~ said target sequence of said oligonucleotide.

146. (Currently Amended) The kit of claim 85, wherein the base sequence of each ~~of~~ said ~~oligonucleotides~~ oligonucleotide is fully complementary to the base sequence of ~~the~~ said target sequence of said oligonucleotide.

147. (Currently Amended) The kit of claim 88, wherein ~~each of said oligonucleotides has a base region which~~ the base sequence of said target binding region of each said oligonucleotide is at least 80% complementary to the base sequence of ~~the~~ said target sequence of said oligonucleotide.

148. (Currently Amended) The kit of claim 88, wherein ~~each of said oligonucleotides has a base region which is 100%~~ the base sequence of said target binding region of each said oligonucleotide is fully complementary to the base sequence of ~~the~~ said target sequence of said oligonucleotide.

149. (Currently Amended) The kit of claim 88, wherein the base sequence of each ~~of~~ said ~~oligonucleotides~~ oligonucleotide is at least 80% complementary to the base sequence of ~~the~~ said target sequence of said oligonucleotide.

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150. (Currently Amended) The kit of claim 88, wherein the base sequence of each ~~of~~ said ~~oligonucleotides~~ oligonucleotide is fully complementary to the base sequence of ~~the~~ said target sequence of said oligonucleotide.

151. (Currently Amended) The kit of claim 88 further comprising a third oligonucleotide, ~~wherein said third oligonucleotide has an at least 10 contiguous base region which is at least 80% complementary to an at least 10 contiguous base region present in~~ from 18 to 35 bases in length that hybridizes to a target sequence ~~contained~~ present in target nucleic acid derived from a *Cryptosporidium* ~~organism~~ organisms under said conditions, ~~and wherein the~~ said target sequence being ~~of said third oligonucleotide~~ is selected from the group consisting of SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26 and SEQ ID NO:28.

152. (Currently Amended) The kit of claim 151, wherein ~~each of said oligonucleotides has a base region which~~ the base sequence of said target binding region of each said oligonucleotide is at least 80% complementary to the base sequence of ~~the~~ said target sequence of said oligonucleotide.

153. (Currently Amended) The kit of claim 151, wherein ~~each of said oligonucleotides has a base region which is 100%~~ the base sequence of said target binding region of each said oligonucleotide is fully complementary to the base sequence of ~~the~~ said target sequence of said oligonucleotide.

154. (Currently Amended) The kit of claim 151, wherein the base sequence of each ~~of~~ said ~~oligonucleotides~~ oligonucleotide is at least 80% complementary to the base sequence of ~~the~~ said target sequence of said oligonucleotide.

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155. (Currently Amended) The kit of claim 151, wherein the base sequence of each ~~of~~ said ~~oligonucleotides~~ oligonucleotide is fully complementary to the base sequence of ~~the~~ said target sequence of said oligonucleotide.

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